



#6

SEQUENCE LISTING

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<120> Slo2 and Slo4, Novel Potassium Channel Proteins from
Human Brain

<130> 018512-006810US

<140> US 09/921,159

<141> 2001-08-01

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<151> 2000-11-15

<160> 38

<170> PatentIn Ver. 2.1

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565 570 575	
tcg ttt tat cat gga cct tcc aga tta cct gta cat agc ata att gcc	1776
Ser Phe Tyr His Gly Pro Ser Arg Leu Pro Val His Ser Ile Ile Ala	
580 585 590	
agc atg ggt act gtg gct ata gac ttg caa gat aca agc tgt aga tca	1824
Ser Met Gly Thr Val Ala Ile Asp Leu Gln Asp Thr Ser Cys Arg Ser	
595 600 605	
gca agt ggc cct acc ctg tct ctt cct aca gag gga agc aaa gaa ata	1872
Ala Ser Gly Pro Thr Leu Ser Leu Pro Thr Glu Gly Ser Lys Glu Ile	
610 615 620	
aga aga cct agc att gct cct gtt tta gag gtt gca gat aca tca tcg	1920
Arg Arg Pro Ser Ile Ala Pro Val Leu Glu Val Ala Asp Thr Ser Ser	
625 630 635 640	
att caa aca tgt gat ctt cta agt gac caa tca gaa gat gaa act aca	1968
Ile Gln Thr Cys Asp Leu Leu Ser Asp Gln Ser Glu Asp Glu Thr Thr	
645 650 655	
cca gat gaa gaa atg tct tca aac tta gag tat gct aaa ggt tac cca	2016
Pro Asp Glu Glu Met Ser Ser Asn Leu Glu Tyr Ala Lys Gly Tyr Pro	
660 665 670	
cct tat tct cca tat ata gga agt tca ccc act ttt tgt cat ctc ctt	2064
Pro Tyr Ser Pro Tyr Ile Gly Ser Ser Pro Thr Phe Cys His Leu Leu	
675 680 685	
cat gaa aaa gta cca ttt tgc tgc tta aga tta gac aag agt tgc caa	2112
His Glu Lys Val Pro Phe Cys Cys Leu Arg Leu Asp Lys Ser Cys Gln	
690 695 700	
cat aac tac tat gag gat gca aaa gcc tat gga ttc aaa aat aaa cta	2160
His Asn Tyr Tyr Glu Asp Ala Lys Ala Tyr Gly Phe Lys Asn Lys Leu	
705 710 715 720	
att ata gtt gca gct gaa aca gct gga aat gga tta tat aac ttt att	2208
Ile Ile Val Ala Ala Glu Thr Ala Gly Asn Gly Leu Tyr Asn Phe Ile	
725 730 735	
gtt cct ctc agg gca tat tat aga cca aag aaa gaa ctt aat ccc ata	2256
Val Pro Leu Arg Ala Tyr Tyr Arg Pro Lys Lys Glu Leu Asn Pro Ile	
740 745 750	
gta ctg cta ttg gat aac ccg cca gat atg cat ttt ctg gat gca atc	2304
Val Leu Leu Leu Asp Asn Pro Pro Asp Met His Phe Leu Asp Ala Ile	
755 760 765	
tgt tgg ttt cca atg gtt tac tac atg gtg ggc tct att gac aac cta	2352
Cys Trp Phe Pro Met Val Tyr Tyr Met Val Gly Ser Ile Asp Asn Leu	
770 775 780	

gat gac tta ctc agg tgt gga gtg act ttt gct gct aat atg gtg gtt Asp Asp Leu Leu Arg Cys Gly Val Thr Phe Ala Ala Asn Met Val Val 785 790 795 800	2400
gtg gat aaa gag agc acc atg agt gcc gag gaa gac tac atg gca gat Val Asp Lys Glu Ser Thr Met Ser Ala Glu Glu Asp Tyr Met Ala Asp 805 810 815	2448
gcc aaa acc att gtg aac gtg cag aca ctc ttc agg ttg ttt tcc agt Ala Lys Thr Ile Val Asn Val Gln Thr Leu Phe Arg Leu Phe Ser Ser 820 825 830	2496
ctc agt att atc aca gag cta act cac ccc gcc aac atg aga ttc atg Leu Ser Ile Ile Thr Glu Leu Thr His Pro Ala Asn Met Arg Phe Met 835 840 845	2544
caa ttc aga gcc aaa gac tgt tac tct ctt gct ctt tca aaa ctg gaa Gln Phe Arg Ala Lys Asp Cys Tyr Ser Leu Ala Leu Ser_Lys Leu Glu 850 855 860	2592
aag aaa gaa cgg gag aga ggc tct aac ttg gcc ttt atg ttt cga ctg Lys Lys Glu Arg Glu Arg Gly Ser Asn Leu Ala Phe Met Phe Arg Leu 865 870 875 880	2640
cct ttt gct gct ggg agg gtg ttt agc atc agt atg ttg gac act ctg Pro Phe Ala Ala Gly Arg Val Phe Ser Ile Ser Met Leu Asp Thr Leu 885 890 895	2688
ctg tat cag tca ttt gtg aag gat tat atg att tct atc acg aga ctt Leu Tyr Gln Ser Phe Val Lys Asp Tyr Met Ile Ser Ile Thr Arg Leu 900 905 910	2736
ctg ttg gga ctg gac act aca cca gga tct ggg ttt ctt tgt tct atg Leu Leu Gly Leu Asp Thr Thr Pro Gly Ser Gly Phe Leu Cys Ser Met 915 920 925	2784
aaa atc act gca gat gac tta tgg atc aga act tat gcc aga ctt tat Lys Ile Thr Ala Asp Asp Leu Trp Ile Arg Thr Tyr Ala Arg Leu Tyr 930 935 940	2832
cag aag ttg tgt tct tct act gga gat gtt ccc att gga atc tac agg Gln Lys Leu Cys Ser Ser Thr Gly Asp Val Pro Ile Gly Ile Tyr Arg 945 950 955 960	2880
act gag tct cag aaa ctt act aca tct gag tct caa ata tct atc agt Thr Glu Ser Gln Lys Leu Thr Thr Ser Glu Ser Gln Ile Ser Ile Ser 965 970 975	2928
gta gaa gag tgg gaa gac acc aaa gac tcc aaa gaa caa ggg cac cac Val Glu Glu Trp Glu Asp Thr Lys Asp Ser Lys Glu Gln Gly His His 980 985 990	2976
cgc agc aac cac cgc aac tca aca tcc agt gac cag tcg gac cat ccc Arg Ser Asn His Arg Asn Ser Thr Ser Ser Asp Gln Ser Asp His Pro 995 1000 1005	3024
ttg ctg cgg aga aaa agc atg cag tgg gcc cga aga ctg agc aga aaa Leu Leu Arg Arg Lys Ser Met Gln Trp Ala Arg Arg Leu Ser Arg Lys 1010 1015 1020	3072

ggc cca aaa cac tct ggt aaa aca gct gaa aaa ata acc cag cag cga 3120
 Gly Pro Lys His Ser Gly Lys Thr Ala Glu Lys Ile Thr Gln Gln Arg
 1025 1030 1035 1040
 ctg aac ctc tac agg agg tca gaa aga caa gag ctt gct gaa ctt gtg 3168
 Leu Asn Leu Tyr Arg Arg Ser Glu Arg Gln Glu Leu Ala Glu Leu Val
 1045 1050 1055
 aaa aat aga atg aaa cac ttg ggt ctt tct aca gtg gga tat gat gaa 3216
 Lys Asn Arg Met Lys His Leu Gly Leu Ser Thr Val Gly Tyr Asp Glu
 1060 1065 1070
 atg aat gat cat caa agt acc ctc tcc tac atc ctg att aac cca tct 3264
 Met Asn Asp His Gln Ser Thr Leu Ser Tyr Ile Leu Ile Asn Pro Ser
 1075 1080 1085
 cca gat acc aga ata gag ctg aat gat gtt gta tac tta att cga cca 3312
 Pro Asp Thr Arg Ile Glu Leu Asn Asp Val Val Tyr Leu Ile Arg Pro
 1090 1095 1100
 gat cca ctg gcc tac ctt cca aac agt gag ccc agt cga aga aac agc 3360
 Asp Pro Leu Ala Tyr Leu Pro Asn Ser Glu Pro Ser Arg Arg Asn Ser
 1105 1110 1115 1120
 atc tgc aat gtc act ggt caa gat tct cgg gag gaa act caa ctt tga 3408
 Ile Cys Asn Val Thr Gly Gln Asp Ser Arg Glu Glu Thr Gln Leu
 1125 1130 1135

<210> 4
 <211> 1135
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human Slo4 potassium channel alpha subunit

<400> 4
 Met Val Asp Leu Glu Ser Glu Val Pro Pro Leu Pro Pro Arg Tyr Arg
 1 5 10 15
 Phe Arg Asp Leu Leu Leu Gly Asp Gln Gly Trp Gln Asn Asp Asp Arg
 20 25 30
 Val Gln Val Glu Phe Tyr Met Asn Glu Asn Thr Phe Lys Glu Arg Leu
 35 40 45
 Lys Leu Phe Phe Ile Lys Asn Gln Arg Ser Ser Leu Arg Ile Arg Leu
 50 55 60
 Phe Asn Phe Ser Leu Lys Leu Leu Ser Cys Leu Leu Tyr Ile Ile Arg
 65 70 75 80
 Val Leu Leu Glu Asn Pro Ser Gln Gly Asn Glu Trp Ser His Ile Phe
 85 90 95
 Trp Val Asn Arg Ser Leu Pro Leu Trp Gly Leu Gln Val Ser Val Ala
 100 105 110
 Leu Ile Ser Leu Phe Glu Thr Ile Leu Leu Gly Tyr Leu Ser Tyr Lys
 115 120 125
 Gly Asn Ile Trp Glu Gln Ile Leu Arg Ile Pro Phe Ile Leu Glu Ile
 130 135 140
 Ile Asn Ala Val Pro Phe Ile Ile Ser Ile Phe Trp Pro Ser Leu Arg
 145 150 155 160
 Asn Leu Phe Val Pro Val Phe Leu Asn Cys Trp Leu Ala Lys His Ala
 165 170 175

Leu	Glu	Asn	Met	Ile	Asn	Asp	Leu	His	Arg	Ala	Ile	Gln	Arg	Thr	Gln	
			180					185					190			
Ser	Ala	Met	Phe	Asn	Gln	Val	Leu	Ile	Leu	Ile	Ser	Thr	Leu	Leu	Cys	
		195					200					205				
Leu	Ile	Phe	Thr	Cys	Ile	Cys	Gly	Ile	Gln	His	Leu	Glu	Arg	Ile	Gly	
	210					215					220					
Lys	Lys	Leu	Asn	Leu	Phe	Asp	Ser	Leu	Tyr	Phe	Cys	Ile	Val	Thr	Phe	
225					230					235					240	
Ser	Thr	Val	Gly	Phe	Gly	Asp	Val	Thr	Pro	Glu	Thr	Trp	Ser	Ser	Lys	
				245					250					255		
Leu	Phe	Val	Val	Ala	Met	Ile	Cys	Val	Ala	Leu	Val	Val	Leu	Pro	Ile	
			260					265					270			
Gln	Phe	Glu	Gln	Leu	Ala	Tyr	Leu	Trp	Met	Glu	Arg	Gln	Lys	Ser	Gly	
	275						280					285				
Gly	Asn	Tyr	Ser	Arg	His	Arg	Ala	Gln	Thr	Glu	Lys	His	Val	Val	Leu	
	290					295					300					
Cys	Val	Ser	Ser	Leu	Lys	Ile	Asp	Leu	Leu	Met	Asp	Phe	Leu	Asn	Glu	
305					310					315					320	
Phe	Tyr	Ala	His	Pro	Arg	Leu	Gln	Asp	Tyr	Tyr	Val	Val	Ile	Leu	Cys	
				325					330					335		
Pro	Thr	Glu	Met	Asp	Val	Gln	Val	Arg	Arg	Val	Leu	Gln	Ile	Pro	Met	
			340					345					350			
Trp	Ser	Gln	Arg	Val	Ile	Tyr	Leu	Gln	Gly	Ser	Ala	Leu	Lys	Asp	Gln	
		355					360					365				
Asp	Leu	Leu	Arg	Ala	Lys	Met	Asp	Asp	Ala	Glu	Ala	Cys	Phe	Ile	Leu	
	370					375					380					
Ser	Ser	Arg	Cys	Glu	Val	Asp	Arg	Thr	Ser	Ser	Asp	His	Gln	Thr	Ile	
385					390					395					400	
Leu	Arg	Ala	Trp	Ala	Val	Lys	Asp	Phe	Ala	Pro	Asn	Cys	Pro	Leu	Tyr	
				405					410					415		
Val	Gln	Ile	Leu	Lys	Pro	Glu	Asn	Lys	Phe	His	Ile	Lys	Phe	Ala	Asp	
			420					425					430			
His	Val	Val	Cys	Glu	Glu	Glu	Phe	Lys	Tyr	Ala	Met	Leu	Ala	Leu	Asn	
		435					440					445				
Cys	Ile	Cys	Pro	Ala	Thr	Ser	Thr	Leu	Ile	Thr	Leu	Leu	Val	His	Thr	
	450					455					460					
Ser	Arg	Gly	Gln	Glu	Gly	Gln	Gln	Ser	Pro	Glu	Gln	Trp	Gln	Lys	Met	
465					470					475					480	
Tyr	Gly	Arg	Cys	Ser	Gly	Asn	Glu	Val	Tyr	His	Ile	Val	Leu	Glu	Glu	
				485					490					495		
Ser	Thr	Phe	Phe	Ala	Glu	Tyr	Glu	Gly	Lys	Ser	Phe	Thr	Tyr	Ala	Ser	
			500					505					510			
Phe	His	Ala	His	Lys	Lys	Phe	Gly	Val	Cys	Leu	Ile	Gly	Val	Arg	Arg	
		515					520					525				
Glu	Asp	Asn	Lys	Asn	Ile	Leu	Leu	Asn	Pro	Gly	Pro	Arg	Tyr	Ile	Met	
	530					535					540					
Asn	Ser	Thr	Asp	Ile	Cys	Phe	Tyr	Ile	Asn	Ile	Thr	Lys	Glu	Glu	Asn	
545					550					555					560	
Ser	Ala	Phe	Lys	Asn	Gln	Asp	Gln	Gln	Arg	Lys	Ser	Asn	Val	Ser	Arg	
				565					570					575		
Ser	Phe	Tyr	His	Gly	Pro	Ser	Arg	Leu	Pro	Val	His	Ser	Ile	Ile	Ala	
			580					585					590			
Ser	Met	Gly	Thr	Val	Ala	Ile	Asp	Leu	Gln	Asp	Thr	Ser	Cys	Arg	Ser	
		595					600					605				
Ala	Ser	Gly	Pro	Thr	Leu	Ser	Leu	Pro	Thr	Glu	Gly	Ser	Lys	Glu	Ile	
	610					615					620					
Arg	Arg	Pro	Ser	Ile	Ala	Pro	Val	Leu	Glu	Val	Ala	Asp	Thr	Ser	Ser	
625					630					635					640	
Ile	Gln	Thr	Cys	Asp	Leu	Leu	Ser	Asp	Gln	Ser	Glu	Asp	Glu	Thr	Thr	
				645					650					655		

Pro	Asp	Glu	Glu	Met	Ser	Ser	Asn	Leu	Glu	Tyr	Ala	Lys	Gly	Tyr	Pro	660	665	670
Pro	Tyr	Ser	Pro	Tyr	Ile	Gly	Ser	Ser	Pro	Thr	Phe	Cys	His	Leu	Leu	675	680	685
His	Glu	Lys	Val	Pro	Phe	Cys	Cys	Leu	Arg	Leu	Asp	Lys	Ser	Cys	Gln	690	695	700
His	Asn	Tyr	Tyr	Glu	Asp	Ala	Lys	Ala	Tyr	Gly	Phe	Lys	Asn	Lys	Leu	705	710	715
Ile	Ile	Val	Ala	Ala	Glu	Thr	Ala	Gly	Asn	Gly	Leu	Tyr	Asn	Phe	Ile	725	730	735
Val	Pro	Leu	Arg	Ala	Tyr	Tyr	Arg	Pro	Lys	Lys	Glu	Leu	Asn	Pro	Ile	740	745	750
Val	Leu	Leu	Leu	Asp	Asn	Pro	Pro	Asp	Met	His	Phe	Leu	Asp	Ala	Ile	755	760	765
Cys	Trp	Phe	Pro	Met	Val	Tyr	Tyr	Met	Val	Gly	Ser	Ile	Asp	Asn	Leu	770	775	780
Asp	Asp	Leu	Leu	Arg	Cys	Gly	Val	Thr	Phe	Ala	Ala	Asn	Met	Val	Val	785	790	795
Val	Asp	Lys	Glu	Ser	Thr	Met	Ser	Ala	Glu	Glu	Asp	Tyr	Met	Ala	Asp	805	810	815
Ala	Lys	Thr	Ile	Val	Asn	Val	Gln	Thr	Leu	Phe	Arg	Leu	Phe	Ser	Ser	820	825	830
Leu	Ser	Ile	Ile	Thr	Glu	Leu	Thr	His	Pro	Ala	Asn	Met	Arg	Phe	Met	835	840	845
Gln	Phe	Arg	Ala	Lys	Asp	Cys	Tyr	Ser	Leu	Ala	Leu	Ser	Lys	Leu	Glu	850	855	860
Lys	Lys	Glu	Arg	Glu	Arg	Gly	Ser	Asn	Leu	Ala	Phe	Met	Phe	Arg	Leu	865	870	875
Pro	Phe	Ala	Ala	Gly	Arg	Val	Phe	Ser	Ile	Ser	Met	Leu	Asp	Thr	Leu	885	890	895
Leu	Tyr	Gln	Ser	Phe	Val	Lys	Asp	Tyr	Met	Ile	Ser	Ile	Thr	Arg	Leu	900	905	910
Leu	Leu	Gly	Leu	Asp	Thr	Thr	Pro	Gly	Ser	Gly	Phe	Leu	Cys	Ser	Met	915	920	925
Lys	Ile	Thr	Ala	Asp	Asp	Leu	Trp	Ile	Arg	Thr	Tyr	Ala	Arg	Leu	Tyr	930	935	940
Gln	Lys	Leu	Cys	Ser	Ser	Thr	Gly	Asp	Val	Pro	Ile	Gly	Ile	Tyr	Arg	945	950	955
Thr	Glu	Ser	Gln	Lys	Leu	Thr	Thr	Ser	Glu	Ser	Gln	Ile	Ser	Ile	Ser	965	970	975
Val	Glu	Glu	Trp	Glu	Asp	Thr	Lys	Asp	Ser	Lys	Glu	Gln	Gly	His	His	980	985	990
Arg	Ser	Asn	His	Arg	Asn	Ser	Thr	Ser	Ser	Asp	Gln	Ser	Asp	His	Pro	995	1000	1005
Leu	Leu	Arg	Arg	Lys	Ser	Met	Gln	Trp	Ala	Arg	Arg	Leu	Ser	Arg	Lys	1010	1015	1020
Gly	Pro	Lys	His	Ser	Gly	Lys	Thr	Ala	Glu	Lys	Ile	Thr	Gln	Gln	Arg	1025	1030	1035
Leu	Asn	Leu	Tyr	Arg	Arg	Ser	Glu	Arg	Gln	Glu	Leu	Ala	Glu	Leu	Val	1045	1050	1055
Lys	Asn	Arg	Met	Lys	His	Leu	Gly	Leu	Ser	Thr	Val	Gly	Tyr	Asp	Glu	1060	1065	1070
Met	Asn	Asp	His	Gln	Ser	Thr	Leu	Ser	Tyr	Ile	Leu	Ile	Asn	Pro	Ser	1075	1080	1085
Pro	Asp	Thr	Arg	Ile	Glu	Leu	Asn	Asp	Val	Val	Tyr	Leu	Ile	Arg	Pro	1090	1095	1100
Asp	Pro	Leu	Ala	Tyr	Leu	Pro	Asn	Ser	Glu	Pro	Ser	Arg	Arg	Asn	Ser	1105	1110	1115
Ile	Cys	Asn	Val	Thr	Gly	Gln	Asp	Ser	Arg	Glu	Glu	Thr	Gln	Leu		1125	1130	1135

<210> 5
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Slo2
 gene-specific nested RACE PCR amplification sense
 primer oligo 1

 <400> 5
 caccacggag ctcacccacc cttcc 25

 <210> 6
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
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 gene-specific nested 3' RACE PCR amplification
 sense primer oligo 2

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 cgcgtcttca gcatcagcat gttggac 27

 <210> 7
 <211> 28
 <212> DNA
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 <220>
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 gene-specific nested 5' RACE PCR amplification
 antisense primer oligo 3

 <400> 7
 ctggtagagc agtgtgtcca acatgctg 28

 <210> 8
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
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 nested 5' RACE PCR amplification antisense primer
 oligo 4

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 actgcatgaa gcgcatgttg gaaggggtg 28

 <210> 9
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<220>
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 gene-specific nested 5' RACE PCR amplification
 antisense primer oligo 5

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<210> 10
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<220>
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 gene-specific nested 5' RACE PCR amplification
 antisense primer oligo 6

<400> 10
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<210> 11
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<220>
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 Slo2-specific 5' PCR amplification antisense
 primer oligo 7

<400> 11
 cacaccacgt ggtcagcaaa cttgacg 27

<210> 12
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
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 Slo2-specific 5' PCR amplification antisense
 primer oligo 8

<400> 12
 gcagttgggg gcgaagtcct tcacgg 26

<210> 13
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Slo2 overlap
 extension PCR amplification sense primer oligo 9

<400> 13
 caccttcaag gagcggctca agctg 25

<210> 14
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Slo2 overlap
 extension PCR amplification antisense primer oligo
 10

<400> 14
 gacgtgtgca ccagcagggt gatgag 26

<210> 15
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Slo2 overlap
 extension PCR amplification sense primer oligo 11

<400> 15
 gtttcacgtc aagtttgctg accacg 26

<210> 16
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Slo2 overlap
 extension PCR amplification antisense primer oligo
 12

<400> 16
 ccgtacgtgc ggatccacag gtcg 24

<210> 17
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Slo2
 amplification sense primer oligo 13

<400> 17
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<210> 18
 <211> 27
 <212> DNA
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 <220>
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 extension PCR amplification antisense primer oligo
 14

 <400> 18
 ttagagctgt gtctcgtcgc gagtctc 27

 <210> 19
 <211> 17
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 <220>
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 <400> 19
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 <210> 20
 <211> 25
 <212> DNA
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 <220>
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 amplification antisense primer oligo 16

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 <210> 21
 <211> 25
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 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Slo2
 amplification primer oligo 17

 <400> 21
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 <210> 22
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
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 amplification primer oligo 18

<400> 22
 gctcccagat gttgcctttg tagctg 26

<210> 23
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Slo4
 amplification sense primer oligo 19

<400> 23
 ggcgtctgct tgattggtgt tagga 25

<210> 24
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Slo4
 amplification antisense primer oligo 20
 overlapping the stop codon in the EST sequence

<400> 24
 atcaaagttg agtttcctcc cgag 24

<210> 25
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Slo4-specific
 5' RACE PCR amplification antisense primer oligo
 21

<400> 25
 cccggagcat ctaccgtaca tcttc 25

<210> 26
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Slo4-specific
 nested 5' RACE PCR amplification antisense primer
 oligo 22

<400> 26
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<210> 27
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
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 Artificial SequenceSlo4-specific 5' RACE PCR
 amplification antisense primer oligo 23

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 gcttggagga ccatgtttca ggagt 25

 <210> 28
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Slo4
 amplification sense primer oligo 24 overlapping
 the initiator Met codon

 <400> 28
 atggttgatt tggagagcga agtg 24

 <210> 29
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
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 amplification sense primer oligo 25

 <400> 29
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 <210> 30
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Slo4-specific
 amplification sense primer oligo 26

 <400> 30
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 <210> 31
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Slo4-specific
amplification antisense primer oligo 27

<400> 31

catctgggtgt agtttcatct tctgattgg

29

<210> 32

<211> 1237

<212> PRT

<213> Rattus norvegicus

<220>

<223> rat potassium channel subunit SLACK

<400> 32

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Pro	Gly	Asp	Thr	Pro	Ala	Gly	Ser	Ala	Ala	Pro	Glu	Glu	Pro	His	Gly
			20					25					30		
Leu	Ser	Pro	Leu	Leu	Pro	Thr	Arg	Gly	Gly	Gly	Ser	Val	Gly	Ser	Asp
		35					40					45			
Val	Gly	Gln	Arg	Leu	His	Val	Glu	Asp	Phe	Ser	Leu	Asp	Ser	Ser	Leu
	50					55					60				
Ser	Gln	Val	Gln	Val	Glu	Phe	Tyr	Val	Asn	Glu	Asn	Thr	Phe	Lys	Glu
	65				70				75						80
Arg	Leu	Lys	Leu	Phe	Phe	Ile	Lys	Asn	Gln	Arg	Ser	Ser	Leu	Arg	Ile
			85					90					95		
Arg	Leu	Phe	Asn	Phe	Ser	Leu	Lys	Leu	Leu	Thr	Cys	Leu	Leu	Tyr	Ile
			100					105					110		
Val	Arg	Val	Leu	Leu	Asp	Asn	Pro	Asp	Gln	Gly	Ile	Gly	Cys	Trp	Gly
	115						120					125			
Cys	Thr	Lys	Tyr	Asn	Tyr	Thr	Phe	Asn	Gly	Ser	Ser	Ser	Glu	Phe	His
	130					135					140				
Trp	Ala	Pro	Ile	Leu	Trp	Val	Glu	Arg	Lys	Met	Ala	Leu	Trp	Val	Ile
	145				150					155					160
Gln	Val	Ile	Val	Ala	Thr	Ile	Ser	Phe	Leu	Glu	Thr	Met	Leu	Leu	Ile
			165						170				175		
Tyr	Leu	Ser	Tyr	Lys	Gly	Asn	Ile	Trp	Glu	Gln	Ile	Phe	His	Val	Ser
			180					185					190		
Phe	Val	Leu	Glu	Met	Ile	Asn	Thr	Leu	Pro	Phe	Ile	Ile	Thr	Val	Phe
	195						200					205			
Trp	Pro	Pro	Leu	Arg	Asn	Leu	Phe	Ile	Pro	Val	Phe	Leu	Asn	Cys	Trp
	210					215					220				
Leu	Ala	Lys	His	Ala	Leu	Glu	Asn	Met	Ile	Asn	Asp	Phe	His	Arg	Ala
	225				230					235					240
Ile	Leu	Arg	Thr	Gln	Ser	Ala	Met	Phe	Asn	Gln	Val	Leu	Ile	Leu	Phe
			245						250				255		
Cys	Thr	Leu	Leu	Cys	Leu	Val	Phe	Thr	Gly	Thr	Cys	Gly	Ile	Gln	His
		260						265					270		
Leu	Glu	Arg	Ala	Gly	Gly	Asn	Leu	Asn	Leu	Leu	Thr	Ser	Phe	Tyr	Phe
	275					280					285				
Cys	Ile	Val	Thr	Phe	Ser	Thr	Val	Gly	Phe	Gly	Asp	Val	Thr	Pro	Lys
	290					295					300				
Ile	Trp	Pro	Ser	Gln	Leu	Leu	Val	Val	Ile	Leu	Ile	Cys	Val	Thr	Leu
	305				310				315						320
Val	Val	Leu	Pro	Leu	Gln	Phe	Glu	Glu	Leu	Val	Tyr	Leu	Trp	Met	Glu
			325						330					335	
Arg	Gln	Lys	Ser	Gly	Gly	Asn	Tyr	Ser	Arg	His	Arg	Ala	Arg	Thr	Glu
			340					345					350		

Lys	His	Val	Val	Leu	Cys	Val	Ser	Ser	Leu	Lys	Ile	Asp	Leu	Leu	Met	355	360	365
Asp	Phe	Leu	Asn	Glu	Phe	Tyr	Ala	His	Pro	Arg	Leu	Gln	Asp	Tyr	Tyr	370	375	380
Val	Val	Ile	Leu	Cys	Pro	Ser	Glu	Met	Asp	Val	Gln	Val	Arg	Arg	Val	385	390	395
Leu	Gln	Ile	Pro	Leu	Trp	Ser	Gln	Arg	Val	Ile	Tyr	Leu	Gln	Gly	Ser	405	410	415
Ala	Leu	Lys	Asp	Gln	Asp	Leu	Met	Arg	Ala	Lys	Met	Asp	Asn	Gly	Glu	420	425	430
Ala	Cys	Phe	Ile	Leu	Ser	Ser	Arg	Asn	Glu	Val	Asp	Arg	Thr	Ala	Ala	435	440	445
Asp	His	Gln	Thr	Ile	Leu	Arg	Ala	Trp	Ala	Val	Lys	Asp	Phe	Ala	Pro	450	455	460
Asn	Cys	Pro	Leu	Tyr	Val	Gln	Ile	Leu	Lys	Pro	Glu	Asn	Lys	Phe	His	465	470	475
Val	Lys	Phe	Ala	Asp	His	Val	Val	Cys	Glu	Glu	Glu	Cys	Lys	Tyr	Ala	485	490	495
Met	Leu	Ala	Leu	Asn	Cys	Ile	Cys	Pro	Ala	Thr	Ser	Thr	Leu	Ile	Thr	500	505	510
Leu	Leu	Val	His	Thr	Ser	Arg	Gly	Gln	Glu	Gly	Gln	Glu	Ser	Pro	Glu	515	520	525
Gln	Trp	Gln	Arg	Met	Tyr	Gly	Arg	Cys	Ser	Gly	Asn	Glu	Val	Tyr	His	530	535	540
Ile	Arg	Met	Gly	Asp	Ser	Lys	Phe	Phe	Arg	Glu	Tyr	Glu	Gly	Lys	Ser	545	550	555
Phe	Thr	Tyr	Ala	Ala	Phe	His	Ala	His	Lys	Lys	Tyr	Gly	Val	Cys	Leu	565	570	575
Ile	Gly	Leu	Lys	Arg	Glu	Glu	Asn	Lys	Ser	Ile	Leu	Leu	Asn	Pro	Gly	580	585	590
Pro	Arg	His	Ile	Leu	Ala	Ala	Ser	Asp	Thr	Cys	Phe	Tyr	Ile	Asn	Ile	595	600	605
Thr	Lys	Glu	Glu	Asn	Ser	Ala	Phe	Ile	Phe	Lys	Gln	Glu	Glu	Lys	Gln	610	615	620
Asn	Arg	Arg	Gly	Leu	Ala	Gly	Gln	Ala	Leu	Tyr	Glu	Gly	Pro	Ser	Arg	625	630	635
Leu	Pro	Val	His	Ser	Ile	Ile	Ala	Ser	Met	Val	Ala	Met	Asp	Leu	Gln	645	650	655
Asn	Thr	Asp	Cys	Arg	Pro	Ser	Gln	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	660	665	670
Lys	Leu	Thr	Leu	Pro	Thr	Glu	Asn	Gly	Ser	Gly	Ser	Arg	Arg	Pro	Ser	675	680	685
Ile	Ala	Pro	Val	Leu	Glu	Leu	Ala	Asp	Ser	Ser	Ala	Leu	Leu	Pro	Cys	690	695	700
Asp	Leu	Leu	Ser	Asp	Gln	Ser	Glu	Asp	Glu	Val	Thr	Pro	Ser	Asp	Asp	705	710	715
Glu	Gly	Leu	Ser	Val	Val	Glu	Tyr	Val	Lys	Gly	Tyr	Pro	Pro	Asn	Ser	725	730	735
Pro	Tyr	Ile	Gly	Ser	Ser	Pro	Thr	Leu	Cys	His	Leu	Leu	Pro	Val	Lys	740	745	750
Ala	Pro	Phe	Cys	Cys	Leu	Arg	Leu	Asp	Lys	Gly	Cys	Lys	His	Asn	Ser	755	760	765
Tyr	Glu	Asp	Ala	Lys	Ala	Tyr	Gly	Phe	Lys	Asn	Lys	Leu	Ile	Ile	Val	770	775	780
Ser	Ala	Glu	Thr	Ala	Gly	Asn	Gly	Leu	Tyr	Asn	Phe	Ile	Val	Pro	Leu	785	790	795
Arg	Ala	Tyr	Tyr	Arg	Ser	Arg	Arg	Glu	Leu	Asn	Pro	Ile	Val	Leu	Leu	805	810	815
Leu	Asp	Asn	Lys	Pro	Asp	His	His	Phe	Leu	Glu	Ala	Ile	Cys	Cys	Phe	820	825	830

Pro Met Val Tyr Tyr Met Glu Gly Ser Val Asp Asn Leu Asp Ser Leu
 835 840 845
 Leu Gln Cys Gly Ile Ile Tyr Ala Asp Asn Leu Val Val Val Asp Lys
 850 855 860
 Glu Ser Thr Met Ser Ala Glu Glu Asp Tyr Met Ala Asp Ala Lys Thr
 865 870 875 880
 Ile Val Asn Val Gln Thr Met Phe Arg Leu Phe Pro Ser Leu Ser Ile
 885 890 895
 Thr Thr Glu Leu Thr His Pro Ser Asn Met Arg Phe Met Gln Phe Arg
 900 905 910
 Ala Lys Asp Ser Tyr Ser Leu Ala Leu Ser Lys Leu Glu Lys Gln Glu
 915 920 925
 Arg Glu Asn Gly Ser Asn Leu Ala Phe Met Phe Arg Leu Pro Phe Ala
 930 935 940
 Ala Gly Arg Val Phe Ser Ile Ser Met Leu Asp Thr Leu Leu Tyr Gln
 945 950 955 960
 Ser Phe Val Lys Asp Tyr Met Ile Thr Ile Thr Arg Leu Leu Leu Gly
 965 970 975
 Leu Asp Thr Thr Pro Gly Ser Gly Tyr Leu Cys Ala Met Lys Val Thr
 980 985 990
 Glu Asp Asp Leu Trp Ile Arg Thr Tyr Gly Arg Leu Phe Gln Lys Leu
 995 1000 1005
 Cys Ser Ser Ser Ala Glu Ile Pro Ile Gly Ile Tyr Arg Thr Glu Cys
 1010 1015 1020
 His Val Phe Ser Ser Glu Pro His Asp Leu Arg Ala Gln Ser Gln Ile
 1025 1030 1035 1040
 Ser Val Asn Met Glu Asp Cys Glu Asp Thr Arg Glu Ala Lys Gly Pro
 1045 1050 1055
 Trp Gly Thr Arg Ala Ala Ser Gly Gly Gly Ser Thr His Gly Arg His
 1060 1065 1070
 Gly Gly Ser Ala Asp Pro Val Glu His Pro Leu Leu Arg Arg Lys Ser
 1075 1080 1085
 Leu Gln Trp Ala Arg Lys Leu Ser Arg Lys Ser Ser Lys Gln Ala Gly
 1090 1095 1100
 Lys Ala Pro Met Thr Thr Asp Trp Ile Thr Gln Gln Arg Leu Ser Leu
 1105 1110 1115 1120
 Tyr Arg Arg Ser Glu Arg Gln Glu Leu Ser Glu Leu Val Lys Asn Arg
 1125 1130 1135
 Met Lys His Leu Gly Leu Pro Thr Thr Gly Tyr Glu Asp Val Ala Asn
 1140 1145 1150
 Leu Thr Ala Ser Asp Val Met Asn Arg Val Asn Leu Gly Tyr Leu Gln
 1155 1160 1165
 Asp Glu Met Asn Asp His His Gln Asn Thr Leu Ser Tyr Val Leu Ile
 1170 1175 1180
 Asn Pro Pro Pro Asp Thr Arg Leu Glu Pro Asn Asp Ile Val Tyr Leu
 1185 1190 1195 1200
 Ile Arg Ser Asp Pro Leu Ala His Val Thr Ser Ser Ser Gln Ser Arg
 1205 1210 1215
 Lys Ser Ser Cys Ser Asn Lys Leu Ser Ser Cys Asn Pro Glu Thr Arg
 1220 1225 1230
 Asp Glu Thr Gln Leu
 1235

<210> 33

<211> 1151

<212> PRT

<213> Homo sapiens

<220>

<223> partial human cDNA KIAA1422

26

27

Ser Leu Ala Leu Ser Lys Leu Glu Lys Arg Glu Arg Glu Asn Gly Ser
 965 970 975
 Asn Leu Ala Phe Met Phe Arg Leu Pro Phe Ala Ala Gly Arg Val Phe
 980 985 990
 Ser Ile Ser Met Leu Asp Thr Leu Leu Tyr Gln Ser Phe Val Lys Asp
 995 1000 1005
 Tyr Met Ile Thr Ile Thr Arg Leu Leu Leu Gly Leu Asp Thr Thr Pro
 1010 1015 1020
 Gly Ser Gly Tyr Leu Cys Ala Met Lys Ile Thr Glu Gly Asp Leu Trp
 1025 1030 1035 1040
 Ile Arg Thr Tyr Gly Arg Leu Phe Gln Lys Leu Cys Ser Ser Ser Ala
 1045 1050 1055
 Glu Ile Pro Ile Gly Ile Tyr Arg Thr Glu Ser His Val Phe Ser Thr
 1060 1065 1070
 Ser Glu Pro His Asp Leu Arg Ala Gln Ser Gln Ile Ser Val Asn Val
 1075 1080 1085
 Glu Asp Cys Glu Asp Thr Arg Glu Val Lys Gly Pro Trp Gly Ser Arg
 1090 1095 1100
 Ala Gly Thr Gly Gly Ser Ser Gln Gly Arg His Thr Gly Gly Gly Asp
 1105 1110 1115 1120
 Pro Ala Glu His Pro Leu Leu Arg Arg Lys Ser Leu Gln Trp Ala Arg
 1125 1130 1135
 Arg Leu Ser Arg Lys Ala Pro Lys Gln Ala Gly Arg Ala Ala Ala
 1140 1145 1150

<210> 34
 <211> 200
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:poly Gly
 flexible linker

<220>
 <221> MOD_RES
 <222> (6)..(200)
 <223> Gly at positions 6-200 may be present or absent

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 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 1 5 10 15
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 20 25 30
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 35 40 45
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 50 55 60
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 65 70 75 80
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 85 90 95
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 100 105 110
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 115 120 125
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 130 135 140
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 145 150 155 160

<220>

<223> Description of Artificial Sequence:Slo4
amplification sense primer oligo 24 overlapping
the initiator Met codon and 5' MunI site for
subcloning and Kozak consensus sequence

<400> 38

atcccaattg ccgccatggt tgatttggag agcgaagtg

39